Adaptive active contours (snakes) for the segmentation of complex structures in biological images

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ABSTRACT

The rapidly evolving field of biological imaging has seen the recent advent of several technologies that yield three-dimensional images of cells, tissues, organs and organisms. As a result, huge volumes of image data are now routinely produced. Automatized tools are hence required to help users process and analyze efficiently their data. Image segmentation is a key step that is both difficult and time-consuming if performed manually. Unfortunately, fully automatic segmentation approaches generally behave poorly on biological images because of low local contrasts, high noise levels and numerous structures or artifacts surrounding the objects of interest. In that context, methods incorporating *a priori* knowledge and allowing user-guidance are more suited. Among these, active contours (also known as snakes) have received a particular attention. Snakes combine image data and elasticity constraints to iteratively refine an initial, coarsely located contour. However, the elasticity constraints and the gradient-based driving forces generally prevent snakes to enter into invaginated structures and correctly follow their contours. We present a new snake model based on a geometrical approach that circumvents this limitation by displacing the snake vertices along their normals towards the closest candidate edges, while avoiding neighboring vertices to move too far away from each other. The key issue for the successful application of this new snake model is the tuning of the parameters controlling its rigidity. In particular, we observed that it is often beneficial to let the elasticity constraints vary with time. However, the optimal temporal profile cannot be specified beforehand. We thus propose an adaptive scheme that automatically adjusts the rigidity of the snake during its evolution towards an image contour. The new method called AB-Snake is available as a plugin for ImageJ. It can segment complex structures in 2D images as well as 3D or temporal images. The plugin is available at http://www.snv.jussieu.fr/~wboudier/softs.html.

Keywords: active contours, segmentation, ImageJ.

1. INTRODUCTION

Biological imaging is a rapidly evolving field that has seen the recent advent of a number of three-dimensional techniques such as confocal microscopy,[1] magnetic resonance microscopy,[2] micro-computed tomography[3] or electron tomography[4] that yield images of biological specimens at various scales from molecular complexes to organisms. High-throughput processing and analyzing schemes are required to cope with the large volumes of image data that can now be routinely produced. Image segmentation, whereby the contours of the structures of interest are determined, has long been recognized as one of the most important and most difficult step in image analysis. Manual segmentation is time consuming and suffers from both intra- and inter-operator variability. As an alternative, numerous automatic segmentation methods have been developed. However, biological images generally present high noise levels, poor local contrasts and numerous structures or artifacts that surround the objects of interest. Consequently, it is not possible to extract the desired contours using fully automatic segmentation methods.

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In this context, semi-automatic methods are particularly attractive because they allow user intervention for structure selection and ambiguity resolution. Among these, active contours (also known as active contours), are iterative methods that refine an initial, user-provided coarse delineation of an object of interest.[5] The final contour position is optimal in the sense that it minimizes an energy functional defined over the space of candidate contours. The energy encompasses a term that favors solutions passing through pixels with high gradient magnitude. Another term enforces regularization of the solution by favoring contours that satisfy geometrical constraints such as smoothness. The evolution of the snake towards its final position is generally driven by the local gradient direction. Thus, snake points are attracted towards nearest candidate contour points. This makes it very difficult, if not impossible, for snakes to follow boundary concavities and enter into structure invaginations.[6] We describe an active contour scheme that circumvents this limitation. The resulting snake is capable of entering invaginations because points are attracted towards locations with high gradient magnitude along a direction perpendicular to the contour.[7] Choosing a set of parameters that yield correct segmentation results is another difficulty when using snakes. On the one hand, low regularization levels are required to capture morphological details. On the other hand, strong regularization is also required, in particular during the first iterations, to converge towards the global shape of the structure of interest and to avoid erratic behavior of the snake. Consequently, the parameters that govern the behavior of the snake should vary during its evolution. We describe an adaptive scheme to dynamically and automatically control these parameters.

2. MATERIAL AND METHODS

Our model mixes two classical approaches of deformable models[8]: deformable curves and classical active contours. In the deformable curves formulation, if a curve is submitted to a deformation vector field, only the normal component of the deformation vector acts on the shape of the curve. The tangential component only generates a re-parameterization of the curve. Classical active contour models, based on a gradient vector fields, tend to move the snake towards the nearest edges. In the case of infoldings, these edges are at the entrance of the invaginated structure. Hence, the model is stuck at the entrance, while it would be interesting to look at the bottom of the cavity. Our model, based on deformation along normals, makes the model attracted not by the truly closest edges but by the nearest edges found perpendicularly to the model, which in the case of infoldings are located inside cavities. As in the classical snake approach, regularization of the model is ensured by the minimization of an internal energy. The final displacement thus results from a compromise between the complete displacement towards the nearest contour along the normal and the satisfaction of the geometrical constraints incorporated into the internal energy.

2.1. Finding the nearest edges

Detecting the contours perpendicularly to the model is required to enter cavities and infoldings. At any time step, the snake is a list of p points $N_1, \ldots, N_p$. Each point N_i is attracted towards the nearest edge along the normal of that point. Edges are detected using the Canny-Deriche operator.[9, 10] Starting from the current position of point N_i, we search along the normal for the nearest pixel having a gradient magnitude above a specified threshold, within a specified distance range in both directions. The difference between this pixel and point N_i is a candidate displacement $\overrightarrow{D_i}$. In the absence of regularization, the new position M_i of point N_i should verify:

$$M_i = N_i + \overrightarrow{D_i} \tag{1}$$

2.2. Regularization

In order to keep the overall shape of the snake as smooth as possible, we minimize the internal energy E_{int}:

$$E_{int} = \int_s (\alpha(s)|v'(s)|^2 + \beta(s)|v''(s)|^2)ds \tag{2}$$

wherein $v(s)$ is the curve and α and β are regularization parameters that vary along the curve. We arbitrarily set $\beta = 0$ to increase computational speed. Our experience is that this does not dramatically affects the results. After discretization of $v(s)$, Equation 2 becomes:

$$E_{int} = \sum_i \alpha_i |M_i - M_{i-1}|^2 \tag{3}$$

Zeroing partial derivatives of Equation 3 yield the following linear system:

$$(\alpha_i + \alpha_{i+1})M_i = \alpha_i M_{i-1} + \alpha_{i+1} M_{i+1}, \qquad i = 1, \ldots, p \qquad (4)$$

This expresses the fact that the internal energy is minimized by configurations such that each M_i is the barycenter of M_{i+1} and M_{i-1} weighted by their α coefficients. However, each new point M_i should also verify Equation 1, that moves the points towards edges. Minimizing for each point M_i attraction towards edges and regularization, the following system results:

$$(\alpha_i^2 + 2\alpha_i \alpha_{i+1} + \alpha_{i+1}^2 + 1)M_i = (\alpha_i \alpha_{i+1} + \alpha_i^2)M_{i-1} + (\alpha_i \alpha_{i+1} + \alpha_{i+1}^2)M_{i+1} + N_i + \overrightarrow{D}_i \qquad (5)$$

When $\alpha = 0$, the new point M_i is simply $N_i + \overrightarrow{D}_i$. When $\alpha \to \infty$, the new point M_i simply equals the barycenter of points M_{i-1} and M_{i+1}. The α parameters can be adjusted to control the balance between the smoothness of the curve and the closeness to the edges. In order to allow the model to enter cavities, points having a high candidate displacement should be less regularized than others: they should be given low α values. On the contrary, points located near edges should be more regularized in order to keep the shape smooth and, therefore, given high α values. This is ensured by the computing αs as follows:

$$\alpha_i = \frac{\lambda}{1 + \mu \overline{D_i}}, \qquad (6)$$

where λ and μ are coefficients for controlling the range of α values and $\overline{D_i}$ is the norm of $\overrightarrow{D_i}$ normalized between 0 and 1.

2.3. Adaptive procedure

To ensure that the snake can adapt to the complex morphology of biological structures, it is important that regularization should not be too strong. However, the user generally initializes the snake with a position and a shape that significantly differ from that of the structure of interest. In that case, too weak a regularization may lead to erratic behavior and noise sensitivity. Thus, regularization parameters should vary with time. However, their optimal temporal evolution cannot be specified beforehand. We thus propose an adaptive scheme to automatically adjust the snake parameters during its evolution towards the final position. Initially, regularization parameters are given high values to guarantee model smoothness and to capture the overall shape of the object. Each time step, the average candidate displacement $\overrightarrow{D}$ is computed. A decreasing of this quantity from one step to the next indicates that the snake is progressing towards edges. In that case, regularization parameters are left unchanged. Alternatively, a stable or increasing $\overrightarrow{D}$ (which may occur due to regularization) is an indication that the snake is probably stuck. In that case, the regularization parameters are decreased for the next iteration. This mechanism allows the snake to progressively enter small infoldings.

In parallel, the smoothing parameter that controls the behavior of the Canny-Deriche gradient operator is also adaptively tuned during the evolution of the snake. Smoothing is important during the first iterations to avoid noise sensitivity. Smoothing is reduced and a new gradient image is computed each time the snake stabilizes. This guarantees that image details are progressively made accessible to the snake in the gradient image. Overall, this strategy mimics a coarse to fine multi-resolution approach.

3. RESULTS AND DISCUSSION

The plugin works with gray-level images and stacks. The user has first to draw a region of interest inside or outside the object he would like to segment. The plug-in will ask, in a basic version, for the gradient threshold used in edge detection, the number of iterations, and various options, like the first and last slice to segment in the case of stacks, the color to display the model, and if the user wants to save the coordinates or create a binarized segmented image. Advanced parameters are also available to set up more parameters such as regularization parameters and the adaptive scheme.

The model is quite versatile since it can either reproduce the classical behavior of snake with high values of regularization, but also can segment very thin and complex structures such as ones present in biological images. Figure 1 illustrates the segmentation of a transverse section in the mouse heart. During the first iterations, the model is quite smooth but does not enter into infoldings. During later iterations, the model is less smooth but enter into infoldings while still being robust to noise.
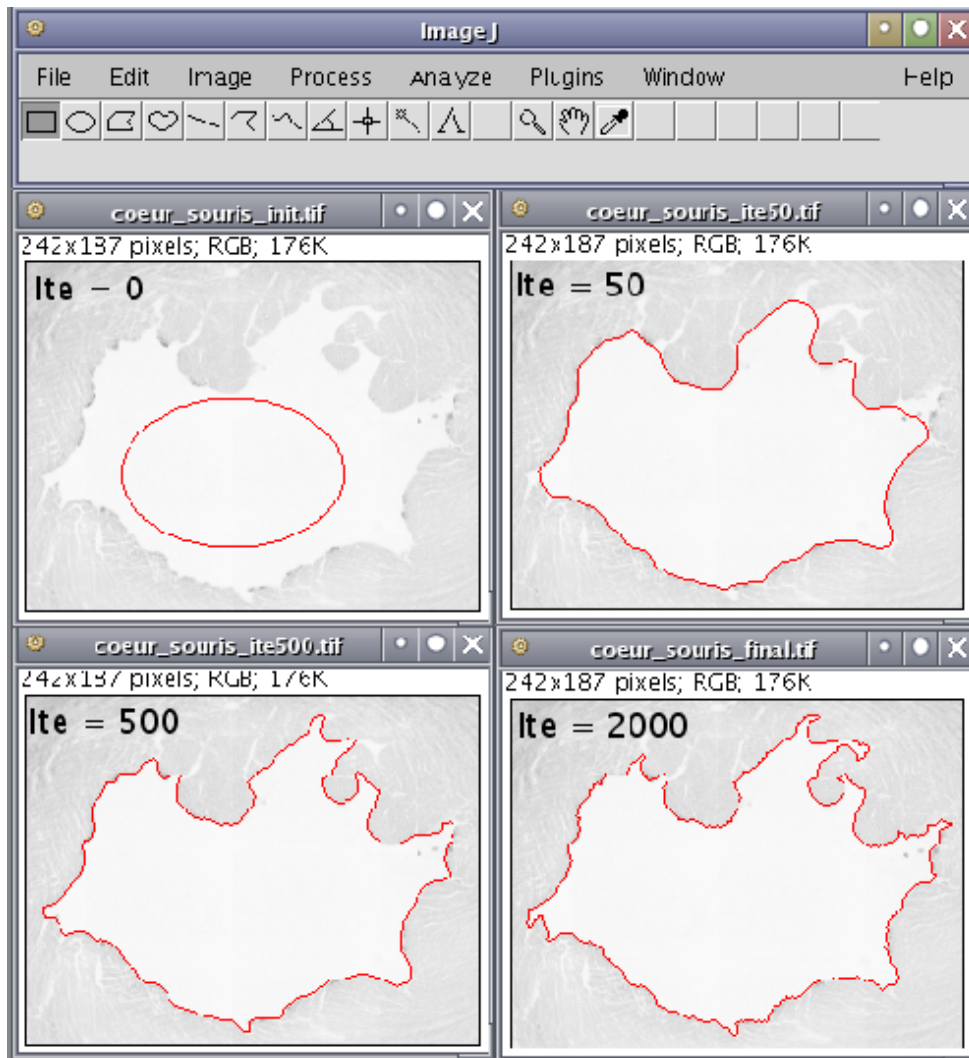
Figure 1. Results of segmentation on a section of a slice of the mouse heart. Starting from a initialization inside the ventricle, the model will deform itself to segment all small infoldings. Displayed are the number of iterations.

4. CONCLUSION

We developed a new active contour model that allows the segmentation of fine structures while being quite robust to noise thanks to an adaptive approach. The algorithm is freely available as an ImageJ plugin at http://www.snv.jussieu.fr/∼wboudier/softs.html.

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